Figure 1

exon II

megsin	ATTGATAAGgtcag (SEQ ID NO: 35)	tacagTTGCTTCAT (SEQ ID NO: 36)
PAI2	ATGGCCAAGgtgag (SEQ ID NO: 47)	tgcagGTGCTTCAG (SEQ ID NO: 48)

exon III

megsin	AATAGTCAGgtaaa (SEQ ID NO: 37)	aacagTCAGGGCTC (SEQ ID NO: 38)
PAI2	ATTTTGCAGgtatc (SEQ ID NO: 49)	tcaagGCACAAGCT (SEQ ID NO: 50)

exon IV

megsin	TTTCATAAGgtaag (SEQ ID NO: 39)	tatagGACTACATT (SEQ ID NO: 40)
PAI2	TTCCGGGAAgtaag (SEQ ID NO: 51)	aaaagGAATATATT (SEQ ID NO: 52)

exon V

megsin	ACATGgtgag (SEQ ID NO: 41)	aaaagGCAAA (SEQ ID NO: 42)
PAI2	CAAACCAAAGgtaaa (SEQ ID NO: 53)	ctgtagGCAAAATCC (SEQ ID NO: 54)

exon IV

megsin	CCAAGgtatg (SEQ ID NO: 43)	ttcagTGCTC (SEQ ID NO: 44)
PAI2	GTAAACTCGgtatg (SEQ ID NO: 55)	attagGCTCAGCGC (SEQ ID NO: 56)

exon IV

megsin	CTGAAgtaag (SEQ ID NO: 45)	tacagATTGA (SEQ ID NO: 46)
PAI2	TTGGAGCTGgtaag (SEQ ID NO: 57)	tgcagCTGGAAAGT (SEQ ID NO: 58)

Figure 2

· Promoter region 1431 bp (-1431~-1)
  (SEQ ID NO: 2)

     -1431

```
        a ctttatatcc tcagtaggta agaaatacaa aggatatggg attcaaaata  -1381
ttcagcctat gaacactgca attagaatat ggagaacagg gaatccattt gtaggctcat  -1321
tttttttta tattaacaac aaccttctcc ttcagaaagt tcaccacaac tgctaaatca  -1261
aaattaaatt tcagggattt tctgcaactt tacttttctc tatgattatt catctcataa  -1201
acaatcatgg aggtgagcaa taactacttt attcgatttt ggataagtta acaggacccc  -1141
cttcttcctg ggaaggaggc aaaattgcac aaaattgaga ggcgagcaac tgtaagatga  -1081
tggtaccttc taattccaat agctttttac aatagagaac ccagttactt ggataaatgt  -1021
tggctgtact tttgaaaaca ctcaggcaga aggaccaggc ttgcagtcat ttccatgcat  -961
agcaggtgaa ggtaggtgca acatacagct caacctcatg atgctacggc cagaaactga  -901
aatgtgtttt tgcccctgtg tggcatgttc tgatggcaaa ggtgtaggca accaactagg  -841
cccaacctac ctttccctac acctggtcac ttttcaaagt gcaaacccac tttaacaaac  -781
tctagcctgt attataggag gaaggatctg ggtggtgcag acgtggcttt ccattgccag  -721
atcagaaggg tggaggagag actggcagga tgacaagaat gaatgaacac accaagtttc  -661
agctcctatc tgaagctgct cagttcaggt aagcatttag agaagccagt tgcaataact  -601
aacagggcaa atgtttctct ggaaaattcc aagccagaga aaattgagaa aaagagggaa  -541
ggatggaaag cagtacaaag agaagccagc tcaaaaggtt agaggtccag atgaaaatct  -481
gagattggag aatgataaaa aacattgtgt gagattctat tttaggtcat tatgctaggg  -421
aaatttacac aggatagggt tgaaagaaat taggctataa gatgagtggc aagttgcaat  -361
aaaatggcac cctaaactca ccaagtcact gttgtcactg ctatcttgcc ttagttgatt  -301
tgatgtctag ttagtctatt tgtgtgtttc tcacagaaga gtatgtcttg acccaggctg  -241
acagatactg ttgattctga aatttgtttt tatggttatg ttaaaaccat tgtcattata  -181
agaaacagag atgggaatat tgcctcctga aatctgattc acatacaaac tgaatgaact  -121
acataacaac caccttagtc agatactact ttgaaacctg gttcaaaacc taaatgctta  -61
taagarrctt gagagacagt gctgtgctct gagtcatagg gaagccatcc cagaagccag  -1
```

· 5'-Untranslated region (5'-UTR) 181 bp (+1~+181)
  (SEQ ID NO: 3)

```
gtctacttat caataagcag ctgcctgtgc agagtgcagg ctgcaccttt ggacagcctt   60
taaaactgaa ttctcagaat tttagaacaa atttttgtct agaaatgctg actttggttc  120
attaggtagt ggtaaaacag gctcccttcg aagctctcct tcatcacctt cctaagtgca  180
t                                                                    181
```
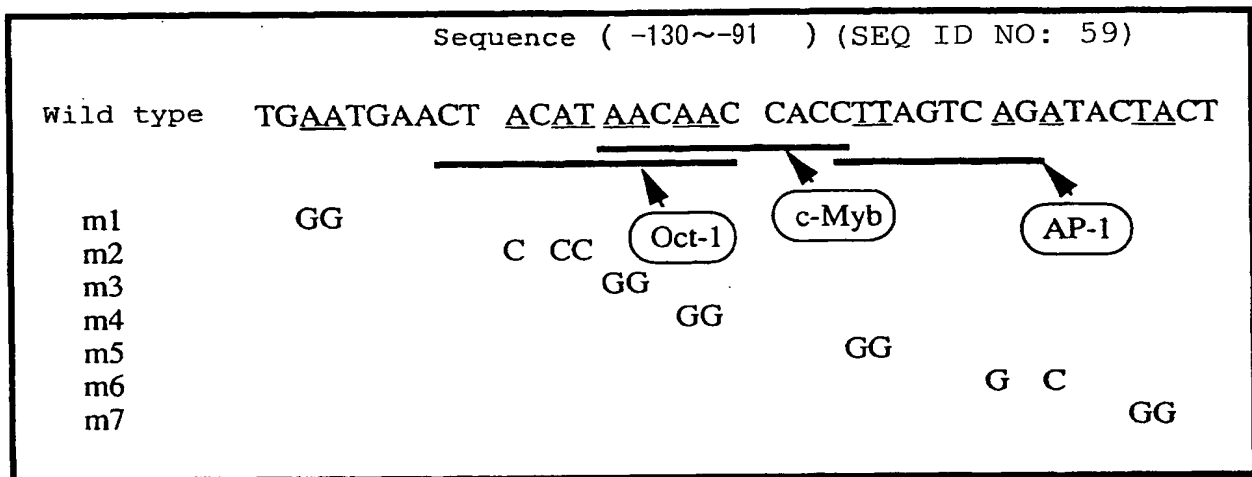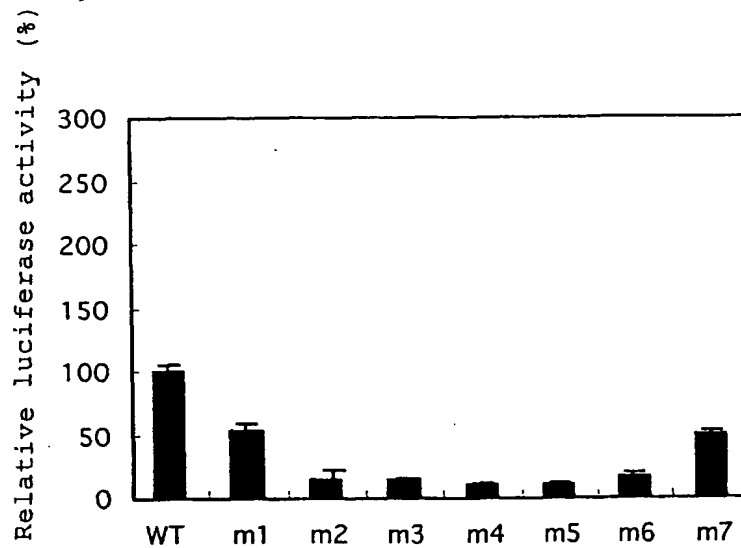
Figure 7

Relative luciferase activity (%)

300
250
200
150
100
50
0

WT   m1   m2   m3   m4   m5   m6   m7

Sequence (-130~-91   ) (SEQ ID NO: 59)

Wild type   TG<u>AA</u>TGAACT <u>ACAT</u> <u>AACAAC</u> CACC<u>TT</u>AGTC <u>AG</u>A<u>TAC</u>T<u>A</u>CT

m1   GG
m2   C CC   Oct-1   c-Myb   AP-1
m3   GG
m4   GG
m5   GG
m6   G   C
m7   GG

Figure 8

Sequence (-130~-89)(SEQ ID NO: 60)

Wild type TGAATGAACT ACAT AACAAC CACCTTAGTC AGATACTACT TT

ProbeA

Probe B

ProbeA ProbeB